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Figure 1: Nucleotide and amino acid sequences (SEQ ID Nos: 1 and 2) of the ATP/ADP translocase from *Chlamydia pneumonia*

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gaaataaaaa actatcagaa tagaaaataa aagtattttca gagggtaaatt atg aca      56
                                     Met Thr
                                     1

aaa acc gaa gaa aaa cct ttt gga aaa ttg cgc tct ttc ttg tgg ccg      104
Lys Thr Glu Glu Lys Pro Phe Gly Lys Leu Arg Ser Phe Leu Trp Pro
                    5                      10                      15

ata cat act cac gag cta aag aaa gtt ctg cca atg ttc cta atg ttc      152
Ile His Thr His Glu Leu Lys Lys Val Leu Pro Met Phe Leu Met Phe
        20                      25                      30

ttc tgt att aca ttt aac tat acg gtg tta cgc gat aca aaa gac act      200
Phe Cys Ile Thr Phe Asn Tyr Thr Val Leu Arg Asp Thr Lys Asp Thr
        35                      40                      45                      50

ctt att gtg gga gct cct ggt tct ggt gca gag gca ata cct ttc atc      248
Leu Ile Val Gly Ala Pro Gly Ser Gly Ala Glu Ala Ile Pro Phe Ile
                    55                      60                      65

aag ttt tgg ctt gtt gtc ccc tgt gct att atc ttt atg ctt att tat      296
Lys Phe Trp Leu Val Val Pro Cys Ala Ile Ile Phe Met Leu Ile Tyr
                    70                      75                      80

gca aag cta agt aat att tta agt aag cag gcc tta ttt tat gca gtg      344
Ala Lys Leu Ser Asn Ile Leu Ser Lys Gln Ala Leu Phe Tyr Ala Val
                    85                      90                      95

gga acg ccc ttt tta att ttc ttt gcc ctg ttc ccg act gta att tat      392
Gly Thr Pro Phe Leu Ile Phe Phe Ala Leu Phe Pro Thr Val Ile Tyr
        100                      105                      110

ccg cta cgc gat gtt tta cat cct aca gaa ttt gct gac cgt tta cag      440
Pro Leu Arg Asp Val Leu His Pro Thr Glu Phe Ala Asp Arg Leu Gln
        115                      120                      125                      130

gcc atc cta cct cca gga ttg cta gga ctc gtt gcc atc tta aga aac      488
Ala Ile Leu Pro Pro Gly Leu Leu Gly Leu Val Ala Ile Leu Arg Asn
                    135                      140                      145

tgg aca ttt gct gca ttt tat gta ctt gct gaa cta tgg gga agc gtc      536
Trp Thr Phe Ala Ala Phe Tyr Val Leu Ala Glu Leu Trp Gly Ser Val
                    150                      155                      160

atg cta tct cta atg ttc tgg gga ttt gct aat gaa att aca aaa atc      584
Met Leu Ser Leu Met Phe Trp Gly Phe Ala Asn Glu Ile Thr Lys Ile
                    165                      170                      175

cac gaa gca aag cgt ttc tac gct ctt ttc ggt atc gga gct aat att      632
His Glu Ala Lys Arg Phe Tyr Ala Leu Phe Gly Ile Gly Ala Asn Ile
                    180                      185                      190

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Figure 1 (continued)

tct tta cta gct tct ggt cgt gca att gtt tgg gct tca aag ttg aga	680
Ser Leu Leu Ala Ser Gly Arg Ala Ile Val Trp Ala Ser Lys Leu Arg	
195 200 205 210	
gct tcc gtt tct gaa ggt gta gat cct tgg gga att tct tta cgt ctt	728
Ala Ser Val Ser Glu Gly Val Asp Pro Trp Gly Ile Ser Leu Arg Leu	
215 220 225	
ttg atg gct atg act att gta tct gga ctt gtt ctt atg gcc agt tac	776
Leu Met Ala Met Thr Ile Val Ser Gly Leu Val Leu Met Ala Ser Tyr	
230 235 240	
tgg tgg atc aat aag aac gta ttg acc gat cct cgc ttc tat aat cca	824
Trp Trp Ile Asn Lys Asn Val Leu Thr Asp Pro Arg Phe Tyr Asn Pro	
245 250 255	
gaa gaa atg caa aag ggg aaa aaa ggt gct aaa cct aaa atg aat atg	872
Glu Glu Met Gln Lys Gly Lys Lys Gly Ala Lys Pro Lys Met Asn Met	
260 265 270	
aaa gat agc ttc ctc tat ctt gat aga tct cct tat att ctt tta tta	920
Lys Asp Ser Phe Leu Tyr Leu Asp Arg Ser Pro Tyr Ile Leu Leu Leu	
275 280 285 290	
act ctc ttg gtt att gcc tat ggt att tgc att aac tta atc gaa gtg	968
Thr Leu Leu Val Ile Ala Tyr Gly Ile Cys Ile Asn Leu Ile Glu Val	
295 300 305	
act tgg aaa agt cag ctg aaa ctg caa tat cct aat atg aat gac tat	1016
Thr Trp Lys Ser Gln Leu Lys Leu Gln Tyr Pro Asn Met Asn Asp Tyr	
310 315 320	
agt gag ttc atg ggg aac ttc tcc ttc tgg act ggc gta gta tcc gta	1064
Ser Glu Phe Met Gly Asn Phe Ser Phe Trp Thr Gly Val Val Ser Val	
325 330 335	
ctt atc atg cta ttt gtt ggt ggt aac gtc att cgt aaa ttt gga tgg	1112
Leu Ile Met Leu Phe Val Gly Gly Asn Val Ile Arg Lys Phe Gly Trp	
340 345 350	
tta act gga gcc cta gtc act cct gtc atg gtt ctc cta aca ggt atc	1160
Leu Thr Gly Ala Leu Val Thr Pro Val Met Val Leu Leu Thr Gly Ile	
355 360 365 370	
gtt ttc ttc gct ctt gtt atc ttt aga aac caa gct tct ggg ctg gtc	1208
Val Phe Phe Ala Leu Val Ile Phe Arg Asn Gln Ala Ser Gly Leu Val	
375 380 385	
gct atg ttc ggt aca act cct ctc atg cta gct gtg gtt gtc gga gct	1256
Ala Met Phe Gly Thr Thr Pro Leu Met Leu Ala Val Val Val Gly Ala	
390 395 400	
ata cag aat att ctt tcg aaa tcc aca aaa tac gct ctc ttt gac tca	1304
Ile Gln Asn Ile Leu Ser Lys Ser Thr Lys Tyr Ala Leu Phe Asp Ser	
405 410 415	

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Figure 1 (continued)

act	aaa	gaa	atg	gcc	tat	atc	cct	ctt	gac	caa	gag	caa	aaa	gtc	aaa	1352
Thr	Lys	Glu	Met	Ala	Tyr	Ile	Pro	Leu	Asp	Gln	Glu	Gln	Lys	Val	Lys	
	420					425					430					
ggt	aag	gct	gct	att	gat	gta	gtt	gcc	gcc	cgc	ttc	gga	aaa	tca	gga	1400
Gly	Lys	Ala	Ala	Ile	Asp	Val	Val	Ala	Ala	Arg	Phe	Gly	Lys	Ser	Gly	
435					440					445					450	
gga	gct	tta	atc	caa	caa	ggt	ttg	ctc	gtt	atc	tgt	gga	agt	att	gga	1448
Gly	Ala	Leu	Ile	Gln	Gln	Gly	Leu	Leu	Val	Ile	Cys	Gly	Ser	Ile	Gly	
				455					460					465		
gct	atg	acc	cct	tat	ctt	gca	gtg	att	ctt	ctt	ttc	atc	att	gct	att	1496
Ala	Met	Thr	Pro	Tyr	Leu	Ala	Val	Ile	Leu	Leu	Phe	Ile	Ile	Ala	Ile	
			470					475					480			
tgg	ttg	gtt	tct	gca	act	aag	tta	aac	aaa	cta	ttc	tta	gcg	cag	tct	1544
Trp	Leu	Val	Ser	Ala	Thr	Lys	Leu	Asn	Lys	Leu	Phe	Leu	Ala	Gln	Ser	
	485						490					495				
gct	ctt	aaa	gaa	caa	gaa	gtg	gct	caa	gaa	gat	tca	gct	cct	gct	tct	1592
Ala	Leu	Lys	Glu	Gln	Glu	Val	Ala	Gln	Glu	Asp	Ser	Ala	Pro	Ala	Ser	
	500					505				510						
tca	tagag	ttgct	tctctt	actc	ttg	ttgatcc	ctacctgctt	tt								1637
Ser																
515																

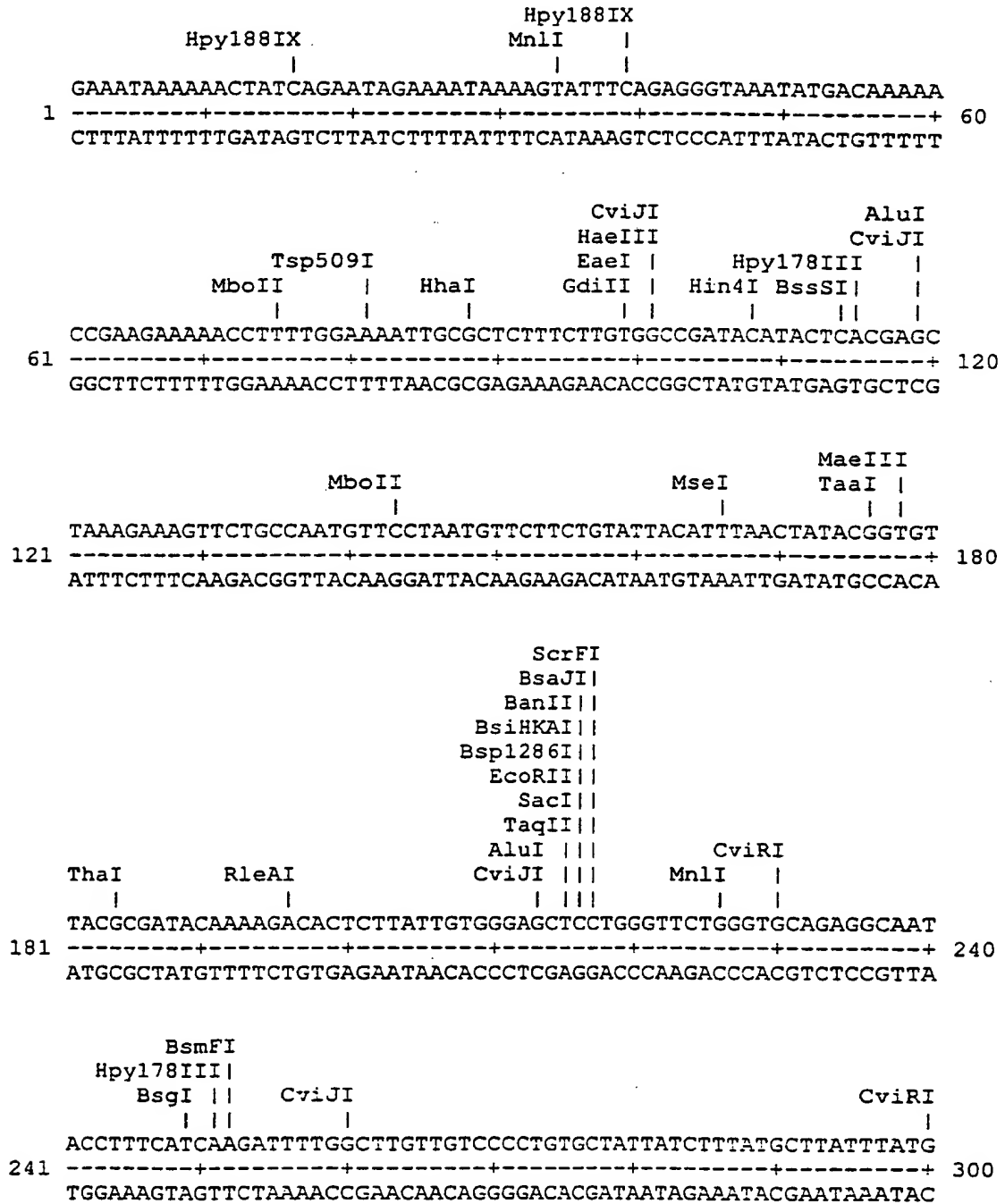
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Figure 2: Restriction enzyme analysis of the *C. pneumoniae* ATP/ADP translocase gene.



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Figure 2 (continued)

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                                CviJI
                                HaeI
                                HaeIII
                                StuI
DdeI      MseI      BtsI
AluI|      SspI|      CviRI|TspRI      MseI
CviJI|      SspI|      Cac8I|      CviRI|TspRI      MseI
||      ||      ||      ||      ||
CAAAGCTAAGTAATATTTTAAGTAAGCAGGCCTTATTTTATGCAGTGGGAACGCCCTTTT
301 -----+-----+-----+-----+-----+-----+-----+ 360
GTTTCGATTCATTATAAAATTCATTTCGTCCGGAATAAAATACGTCACCCCTGCGGGAAAA

                                Tsp509I      ThaI
                                Sth132I|      FokI|
Tsp509I      Hpy178III TaaI|      AciI|      SfcI
|      |      |      |      |
TAATTTTCTTTGCCCTGTTCCCGACTGTAATTTATCCGCTACGCGATGTTTTACATCCTA
361 -----+-----+-----+-----+-----+-----+-----+ 420
ATTAAAGAAACGGGACAAGGGCTGACATTAAATAGGCGATGCGCTACAAAATGTAGGAT

                                BccI
                                CviJI|
                                HaeI|
                                HaeIII|
                                BslI|      CjePI
                                BpmI|      HinfI|
                                CjePI||      BfaI||
ApoI      TaaI|      |      |      ScrFI      MnlI|      |
Tsp509I      FokI|      |      |      EcoRII|      PleI|      |      BccI
|      |      |      |      |      |      |      |
CAGAATTTGCTGACCGTTTACAGGCCATCCTACCTCCAGGATTGCTAGGACTCGTTGCCA
421 -----+-----+-----+-----+-----+-----+-----+ 480
GTCTTAAACGACTGGCAAATGTCCGGTAGGATGGAGGTCCTAACGATCCTGAGCAACGGT

                                MseI      BsrI      CviRI
                                AflIII|      BspGI|      Fnu4HI|      RsaI
                                SmlI|      BbvI|      |      TseI|      |      TatI|      HgaI
                                ||      ||      ||      ||      ||      ||
TCTTAAGAAACTGGACATTTGCTGCATTTTATGTACTTGCTGAACTATGGGGAAGCGTCA
481 -----+-----+-----+-----+-----+-----+-----+ 540
AGAATTCTTTGACCTGTAAACGACGTAAAATACATGAACGACTTGATACCCCTTCGCAGT

                                NlaIII      Tsp509I
                                |      |
TGCTATCTCTAATGTTCTGGGGATTGCTAATGAAATTACAAAAATCCACGAAGCAAAGC
541 -----+-----+-----+-----+-----+-----+-----+ 600
ACGATAGAGATTACAAGACCCCTAAACGATTACTTTAATGTTTTTAGGTGCTTCGTTTCG

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Figure 2 (continued)

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Figure 2 (continued)

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                                                    BglII
                                                    BstYI
                                                    Sau3AI
                                                    AluI
                                                    CviJI
                                                    BfaI
                                                    MnlI
                                                    |||
AGGGGAAAAAAGGTGCTAAACCTAAATGAATATGAAAGATAGCTTCCTCTATCTTGCTA
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
TCCCCTTTTTTTCCACGATTTGGATTTTACTTATACTTTCTATCGAAGGAGATAGAACGAT

                                                    MseI
                                                    CjePI
                                                    MseI
                                                    CviRI
DpnI
AluI
CviJI
GATCTCCTTATATTCTTTTATTAGCTCTCTTGGTTATTGCCTATGGTATTTGCATTAAC
901 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 960
CTAGAGGAATATAAGAAAATAATCGAGAGAACCAATAACGGATACCATAAACGTAATTGA

                                                    CviRI
                                                    MwoI
                                                    CjePI
AluI
CviJI
MaeIII
Tsp45I
TaqI
MspAII
PvuII
SfcI
TAATCGAAGTGACTTGGAAGTCAGCTGAAACTGCAATATCCTAATATGAATGACTATA
961 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020
ATTAGCTTCACTGAACCTTTTCAGTCGACTTTGACGTTATAGGATTATACTTACTGATAT

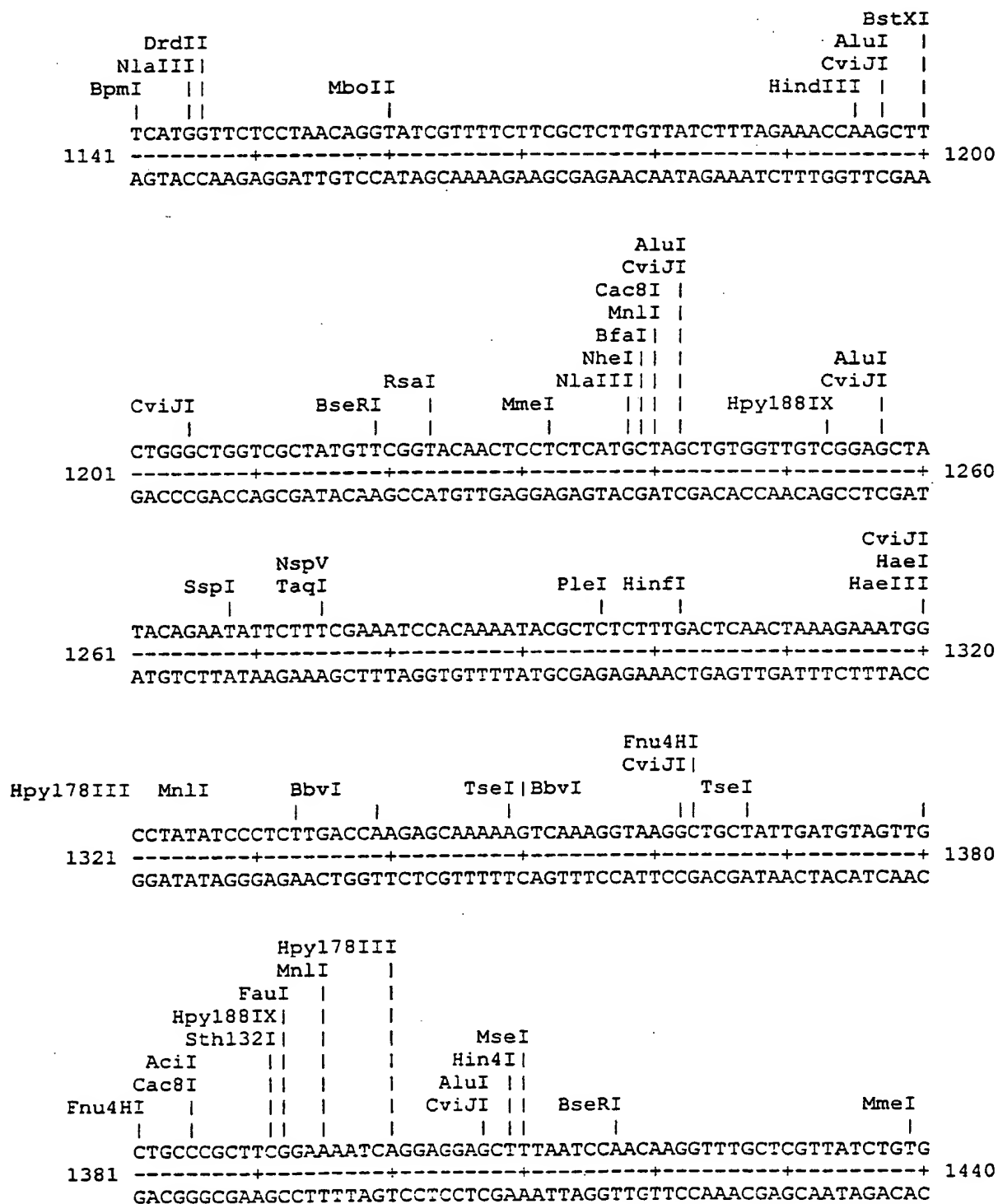
                                                    BspGI
                                                    BciVI
NlaIII
Hpy178III
BsrI
RsaI
NlaIII
GTGAGTTCATGGGGAACCTTCTCCTTCTGGACTGGCGTAGTATCCGTACTTATCATGCTAT
1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080
CACTCAAGTACCCCTTGAAGAGGAAGACCTGACCGCATCATAGGCATGAATAGTACGATA

                                                    MaeIII
                                                    Tsp45I
                                                    BfaI
                                                    BanII
                                                    BsaXI
                                                    Bsp1286I
                                                    Hin4I
                                                    HincII
                                                    CviJI
                                                    HpaI
                                                    BsrI
                                                    MseI
                                                    NlaIV
                                                    FokI
MaeII
MaeIII
Tsp509I
BccI
TTGTTGGTGGTAACGTCATTCGTAAATTGGGATGGTTAACTGGAGCCCTAGTCACTCCTG
1081 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140
AACAACCACCATTCAGTAAGCATTTAACCCTACCAATTGACCTCGGGATCAGTGAGGAC

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Figure 2 (continued)



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Figure 2 (continued)

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                                TspRI
                                HinfI |
                                TfiI |
                                SimI      BtsI | |
                                AluI   |HaeIV   CviRI | | |
                                CviJI   |Hin4I   MboII | | |           BsrDI
                                |   |   |   |   |   |   |   |
1441  GAAGTATTGGAGCTATGACCCCTTATCTTGCAGTGATTCTTCTTTTCATCATTGCTATTT
-----+-----+-----+-----+-----+-----+-----+
CTTCATAACCTCGATACTGGGGAATAGAACGTCACCTAAGAAGAAAAGTAGTAACGATAAA
                                Bce83I
                                DdeI      MwoI   MseI |
                                CviRI   | MseI      DdeI   HhaI   |CjeI   | |
                                |   |   |   |   |   |   |   |
1501  GGTGGGTTTCTGCAACTAAGTTAAACAAACTATTCTTAGCGCAGTCTGCTCTTAAAGAAC
-----+-----+-----+-----+-----+-----+
CCAACCAAAGACGTTGATTCAATTTGTTTGATAAGAATCGCGTCAGACGAGAATTTCTTG
                                AlwNI
                                MboII
                                MboII |
                                Hpy178III   AluI | |
                                SmlI   |HinfI   CviJI | |
                                CviJI | | TfiI   CjeI | | | AceIII
                                ||   |   |   |||   |   |
1561  AAGAAGTGGCTCAAGAAGATTGAGCTCCTGCTTCTTCATAGAGTTGCTTCTCTTACTCTT
-----+-----+-----+-----+-----+-----+
TTCTTCACCGAGTTCTTCTAAGTCGAGGACGAAGAAGTATCTCAACGAAGAGAATGAGAA
                                DpnI
                                Sau3AI |           BspMI
                                | |           |
                                GTTGATCCCTACCTGCTTTT
1621  -----+-----+
CAACTAGGGGATGGACGAAAA

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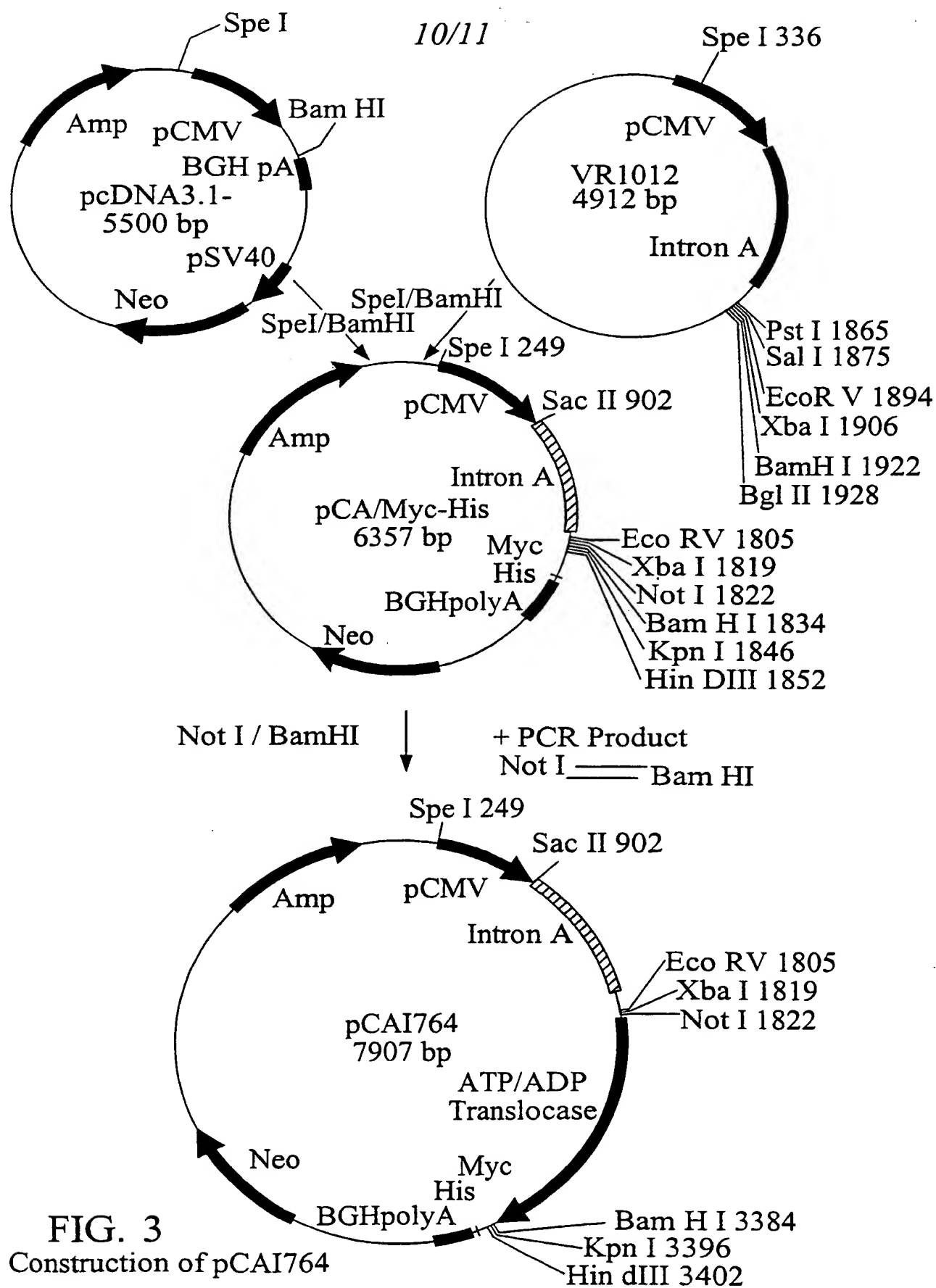


FIG. 3
Construction of pCAI764

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Figure 4: Protective Efficacy of DNA Immunization with pCAI764

